

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable

Application Serial Number:

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

PCT

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/701,001

DATE: 01/11/2001 TIME: 17:02:22

Imput Sot : A:\ES.txt

Output Set: N:\CRF3\01112001\1701001.raw

TIDS APPLICANT: ASAHIKASET KOGYO KABUSHIKI KAISHA ASBRI MEDICAL CO., LED.

Does Not Comply Corrected Diskette Needed

see sen 4 on Enov Summary Sheet

o office within OF INVENTION: Separating apparatus of cells and separating method 8 -130 FILE PEFERUNCE: ASAH: -!

10 <140> CURRENT APPLICATION NUMBER: US/09/701,001 0 (141) CORRENT FILING DATE: 2000-11-22

10 C1912 CHARRY FILING BATE: 2000-11-22
10 C1912 CHARRY FILING BATE: 2000-11-22
11 C1912 CHARRY FILING BATE: 1998-5-25
12 C1512 PRIOR FILING BATE: (1998-5-25) 1998-05-25 (-use this date format
15 C1622 NUMBER OF SEQ TO NOS: 18

ERRORED SEQUENCES

665 <210> SEQ ID NO: 41 666 +2112 LENGTH: (879) 909 shows

568 Kalox OPGANTSM: house

670 4460× SEQUENCE: 41 W--> 673 data aca atg att acg cca age tit gga gcc tit tit tig gag att tic 672 Met. The Met. He Pro See Phe Gly Ata Phe Phe Leu Glu Fle Phe 674 date gig dan aaa tid tid tie gea att ect tid git git ect tie tut 675 Asn val bys Lys Lea Leu Phe Ala Tle Pro Leu Val Val Pro Phe Tyr 676 20 25 30 677 god god can eeg god atg god cag gig aag eig cag cag tet gga cet

678 Ala Ala Gin Pro Ala Net Ala Gin Val Lys Leu Gin Gin Ser Cly Pro 679 35 40 4.5 680 ggc c(a gig cag occ ica cag ago cly ice ito ato igo aca gio ici 681 Gly heu val Gln Pro Ser Gln Ser hen Ser Phe lle Cys Thr Val Ser 55 6.0 G83 ggt tic Lea tto act agt cat ggt gto cac tgg gtt egc cag tel eca 684 GL/ Phe Ser Leu Thr Ser His GLy Val His Trp Val Arg Gln Ser Pro 70 686 yaa aaq ggi olg aag ing olg gga gig ata ing ggi gol gga agg aca

687 Gly Lys Gly heu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr 90 689 yes tot ast yes get the are the aga one age ate age age age att 690 ASP Tyr ASB Ala Ala Phe IIP Ser Arg Len Ser IIe Ser Arg ASP IIe 691 100 105 . 110 692 Loc aag ago caa gil ille iit aag aig ago agi cig caa gil gai gac 693 Ser Lys Ser Glm Val Phe Phe Lys Met Ash Ser Leu Glm Val Asp Asp 695 aca goo ata fat tao tgt goo aga aaf agg tao gag ago tao tti gae 696 Thr Ala Tie Tyc Tyr Cys Ala Arg Asn Acg Tyr Glu Ser Tyr Phe Asp 697 130 135 140

698 tạc tạg gọc cầu ngọ ácc ácg ghe ácc ghe tạc tea gặt gọa gọc gọt 699 Tyr Tup Gly Gin Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

file://C:\CRF3\Outhold\VsrI701001.htm

Imput Set : A:\Es.txt Output Sec: N:\CRF3\01112001\1701001.raw 700 145 70) toa ggo gga gut que not ago ago ago ago ago toa gas uto gay eto act 702 Ser 31, 617 div 617 Ser 617 Cr. 317 div Ser Aspitte 612 Lon 45 703 165 165 170 170 175 704 had bot now obe for ead not give agree the gas gut day ded the abo 705 Clm sor Pro Lem Ser Lea Pic val Ser Lem Gly 280 Glm Ara Ser Lie 1.80 135 100 set the against agricult age of the had but will got as bar 708 Ser Cys Aig Ser Ser Gla Ast tou Val Bis Ser Ast Giv Ast The 1/1 7(7) 195 2016 The trained together organic management god care for any other step and 711 Lew Mis Trp Tyr Lou Sin Les Pro Sir Oth Ser Pro Ash Lew Year He 2.20 713 tur ada gli Lee ado equ itt un ggo gle eva gan agg the agt uge 711 tyr Lys Val Ser Asn ang Phe Ser Guy Val Pro Asp Arg Phe Ser Gly 2 50 2 45 716 agt aga teo gog uca goa the aca ere agg ato age aga gtg gog get 717 Ser Gr. Ser Gry The Gra Pad The Lou Lys tie Ser Arg Val Glu Ala 71.8 245 250 719 gas gat ctg gga oth hat the the tet cas and act cat git een ele 720 Glu Asp Lou Gly Val Try Phe Cas Sor Glu Ser Thr His Val Pro Lea 721 265 270 . 722 and its got god ach and old god cid and sod god god god god god. 727 thi Phe GI; Ala GI; The Lies Va. Glu Len Lis Arg Ala Ala GI; W--> 724 275 285 725 gog dog gla dog tat dog gat dog dig gad dog dig god god bag 726 Sta Pro Val Pro Tyr Pro Asp Pro Leu Jin Pro Ang Ala Ala E--> 727 290-) 295 24500 700 29500 300 $806\ < 22.0 >\ 800\ TD\ NO:\ 44$ 807 <211> GENGTH: 16 805 - Elle Type: PRP 809 -213> OPGANISM: Artificial Sequence 6 810 <220> FEATURE: 811 <223> OTHER INFORMATION: Smino acid sequence of heavy chain CDR-2 813 :400> SEQUENCE: 44 814 Val. Fle Tro Gly Alo Giy Arg Thr Asp Tyr Asn Ala Ala Pho Tle Sor 815 1 5 10 10 15 misabjed nos. - see item You Evan Luman 828 <211 - LENGTH: 16 829 <213> TYPE: PRT 836 <213> OSGANTSM: Artificial Sequence 832 -223> OTHER INFORMATION: Amino acid sequence of light chain CDR-1 834 400> SEQUENCE: 46 835 Arg Ser Ser Gln Asu ben Val His Ser Asu Gly Asu Thr Tyr ben His 836 1 10 15E--> 836 fx ws.

DATE: 01/11/2001

TIME: 17:32:34

RAW SEQUENCE LISTING

PAPENT APPLICATION: US/09/701,001

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PAREM APPLICATION: US/09/701,001

DARE: 98/11/2601 TIME: 17:02:25

Input Set : A:\ES.txt

Output Set: N:\CRP3\01112001\1701001.1aw

Late Signer: Secret Application Books, different September Corona, Application No. nato Higgs of Colorest E. Eng Date differs, Reproceed Correct Filtrag Date Colorest Michael Date Colorest Michael Board Reprocessing Prior Fibric activities - Do. 1988 - December 1988 - Dece Land Bridg C. (fa) String into converted to their gase, BUTTE WAY TRACE T BYTHO Figure P. 122 Cr (43) String data was the day rower case. Fig. 1. The state of the state Light to 12 th (in) Straig data conscribed to remer case. Trial Expenses to Souther to 1 96 A Dec to Dessing B ank Line separates, \$2205 field identifier Esy (R., 12 Co (es) String for a converted to lower case. 1:29 files of the section are converted to tower case.
1:29 files of the section of the separator. 220 field identifier 1:280 to the content of the section 1.25 Hill C: (a) String data converted to lower case.
2.25 Hill C: (a) String data converted to lower case.
2.27 Hill a w 'ssing blank the separator. 2.20 field identified 1.20 S:178 H: The fator. Feature missing. 221 and round for FPO IP-:!)
1.305 H:256 W: Kandator Feature missing. 222 not found for SEO IP-:!) L:300 M:340 v: (40) "n" on "Xaa" used: Posture required, for Sky (Da:14 E:300 M:112 C: (43) Suche data converted to lower case, 1.305 H.203 W. Missing Plank Line separator 220 field identifier 13. (0) H.F. W. GESING WINE Line Scholley 220 living Identified Lists IV.23 W. Francisco. Learner missing, 222 not found for SEQ 16-15 Lists Friend W. Hardstor. Feature missing, 222 now found for SEQ 16-15 Lists Hills U. (45) "n" of "Kaa" used: Feature required, for SEQ 16-15 Lists Hills V. (43) String data converted to lower case. Light H.283 w: Fissing Blank Line separator - 0.200 field identifier 1:329 Will? C: (43) String data converted to lower case, E:328 N:253 W: Hissing Blank Line separator, <2200 field identifier 1.330 Hills C: (43) String data converted to lower case, 6:336 H:28' W: Hissing brank Line separator. <220> field identifica L:340 K:11z d: (48) String data converted to lower case. L:345 K:123 d: Elssing clask Line separator, -220> field identifier E:350 U:112 C: (48) String data converted to lower case. L:356 H:383 W: Hissing Brank Line separator, (220) field identifier L:360 H:713 C: (48) String data converted to lower case, 1:366 H:193 W: Missing Brank Line separator, <230> field identifier 1:370 M:142 C: (48) String data convexted to lower case, E:376 H:283 W: Wissing Blank Line separator, <220> field identifier L:380 H:312 C: (18) String data converted to lower case. L:386 H:283 W: Hissing Blank Line separator, <220> field identitier E:390 M:112 C: (18) String data converted to lower case. E:396 E:283 W: Hissing Blank Line separator, <220> field identifier E:400 F:312 C. (48) String data converted to lower case, L:406 B:283 E: Hissing Blank Line separator, <220> field identifier 6.410 M:112 C: (48) String data converted to lower case, L:416 H:283 W. Rissing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY
PARENT APPLICATION: US/09/701,001

12000: 01/17/1001 THOS: 17:00:25

Imput Set : A:\Es.txt

Curper Set: N:\CRF3\01112001\1701001.raw

L:420 M:117 C: (48) String data converted at lever case. L:426 H:283 r size.cg Black Line separator. - 220% field identifier Listo Milly in (4), during data convert if to rower case, E:136 H:200 as his list blank him separation (E26) field identified hallo Minits in (ad) Sheing data comported to lower case. L:446 M:253 v : M selej blank tim separator, . . des theid aded from FilSe Hills - (43) String data converted to lower case. 1:455 Birds o A ssing Plank Time separator, 220% (Sold Educities Lilbe Riell (: (48) String data converted to lower case. 1:466 M.203 m: M.28.m) dark Line segurator, <2262 field admitter L:476 M:2.2 c. (28) String data content to lower case. E:476 M:283 b: E:ssind Wlank Line separator. <220> freed identifier 1:480 Mill? C: (8) String dida convertes to lower case, 11486 Blo23 W. Dies de Slank line superator. 2007 field identifier L:196 B:192 C. (18) String data converted to lower case L:496 B:284 W. Bissing Block line separator. <220; field identifie: 1:500 H:112 C: (40) String data converted to lower case. 5.552 Milis C: (43) String data converted to lower base. M: 132 Repeated in SeqNo=37 1. 583 M: 112 C: (18) String data converted to lower case. M:112 Repeated in SegNo/38 5:610 H:112 C: (18) String data conterned to lower case, M: 112 Repeated in SeqNo.39 bin41 M:112 C: (18) String data converted to lower case. M:112 Repeater it SeqNo=40 h:671 W:112 C: (48) String data contested to lover case, E:673 Hor36 S: invalid Amino Acid Number to Ocding Region, SEC (D.31 M: 112 Reproted to SegMo-41 E:721 M:335 W: invalid Amino Acid Number in Coding Region. SEC 10:41 1:727 M:336 W: Invalid Amino Acid Number In Coding Region, SEQ 10:41 L:727 M:252 D: No. of Seq. differs, <211-LEMGMH:Input:879 Found:909 SEQ:41 L:735 M:112 C: (48) String data converted to lower case. 5:737 M:336 W: Invalid Amino Acid Mumber in Coding Region, SEQ 10:42 M:111 Repeated in SeqNo-42 T:788 M:330 V: Invalid Amino Acid Number in Coding Region, SEC 10:42 1:791 M:336 W: Invalid Amino Acid Number in Odding Region, SE: TD:42 1.:794 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42 L:800 M:283 W: Bissing Blank Line separator. <2.20> field identifier D:810 M:283 W: Bissing Blank Line separator, <2.20> field identified E:815 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEO 1D:44 L:821 M:283 W: Missing Blank Line separator, <220> field identifier L:831 M:283 M: Missing Blank Line separator, 220> field identifier L:836 M:332 E: (32) Invatid/Missing Amino Acid Numbering, SEQ 10:46 L:842 M:283 W: Hissing Blank Line separator. <220> field identifier L:852 H:283 W: Hissing Blank Line separator, <220> field identified

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,001

695 aca ged ata tat tac tgt ged aga aat agg tad gag agd tad ttt gad 696 Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp

698 tac tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt 699 Tyr Trp Cly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

1.35

DATE: 01/11/2001 TIME: 17:02:22

Input Set : A:\ES.txt

Output Set: N:\CRF3\01112001\I701001.raw

Does Not Comply Corrected Diskette Needed 3 <11.0> APPLICANT: ASAHTKASET KOGYO KABUSHTKI KAISHA ASAHI MEDICAL CO., LTD. 6 <120> TITLE OF INVENTION: Separating apparatus of cells and separating method 8 <130> FILE REFERENCE: ASAHI-1

> 10 <140> CURRENT APPLICATION NUMBER: US/09/701,001

3 > 10 <141> CURRENT FILING DATE: 2000-11-22

10 <150> PRIOR APPLICATION NUMBER: IP 10/159957
WE-> 12 <151> PRIOR FILING DATE: (1998-5-25) 1998-05-25 (-use this date format

15 <160> NUMBER OF SEQ ID NOS: 48

ERRORED SEQUENCES

697 130

```
665 <210> SEQ ID NO: 41 909 shows
      667 <212> TYPE: DNA
      668 <213> ORGANISM: mouse
     670 <400> SEQUENCE: 41
C--> 671 atg acc atg att acg cca agc ttt gga gcc ttt ttt ttg gag att ttc
                                                                                         see Lin 4 on
Eva
Junnary
Sheet
672 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe W--> 673 . 5 10 /0 15 /5 674 aac gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat
     675 Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
     676
                    20
                                              2.5
     677 geg gee eag eeg gee atg gee eag gtg aag etg eag eag tet gga eet
     678 Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
                   35
                                         40
                                                                4.5
     680 ggc cta gtg cag ccc tca cag agc ctg tcc ttc atc tgc aca gtc tct
     681 Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phé Ile Cys Thr Val Ser
             50
                                     55
     683 ggt ttc tca tta act agt cat ggt gta cac tgg gtt cgc cag tct cca
684 Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
     685 65
                                 70
     686 gga aag ggt otg gag tgg otg gga gtg ata tgg ggt got gga agg aca
                                                                                    288
     687 Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
                           85
                                                  90
     689 gae tat aut geu get tte ata tee agu etg age ate age agg gae att
                                                                                    336
     690 Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
                                             105
                                                                   1.10
     692 too aag ago caa git tie til aag atg aac agt eig caa git gat gac
                                                                                    384
     693 Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
                 115
                                        120
                                                               1.25
```

140

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". The rules require that a line not exceed 72 characters in length. This includes spaces. Incorrect Line Length The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs Misaligned Amino Acid between the numbering. It is recommended to delete any tabs and use spacing between the numbers. Numbering Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. Variable Length Sequence(s) ___ __ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. A "bug" in Palentin version 2.0 has caused the <220>-<223> section to be missing from amino acid Patentin ver. 2.0 "bug" _. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. Skipped Sequences Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: . (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. (NEW RULES) <210> sequence id number 400> sequence id number Use of n's or Yaa's. Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Use of <213>Organism are missing this mandatory field or its response. (NEW RULES) Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings. (NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) Patentin ver. 2.0 "bug" Rease do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99